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(54) **METHODS AND MATERIALS FOR ASSESSING ALLELIC IMBALANCE**

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None
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(57) **ABSTRACT**

Methods and systems for detecting allelic imbalance using nucleic acid sequencing are provided.

20 Claims, 3 Drawing Sheets

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Figure 1

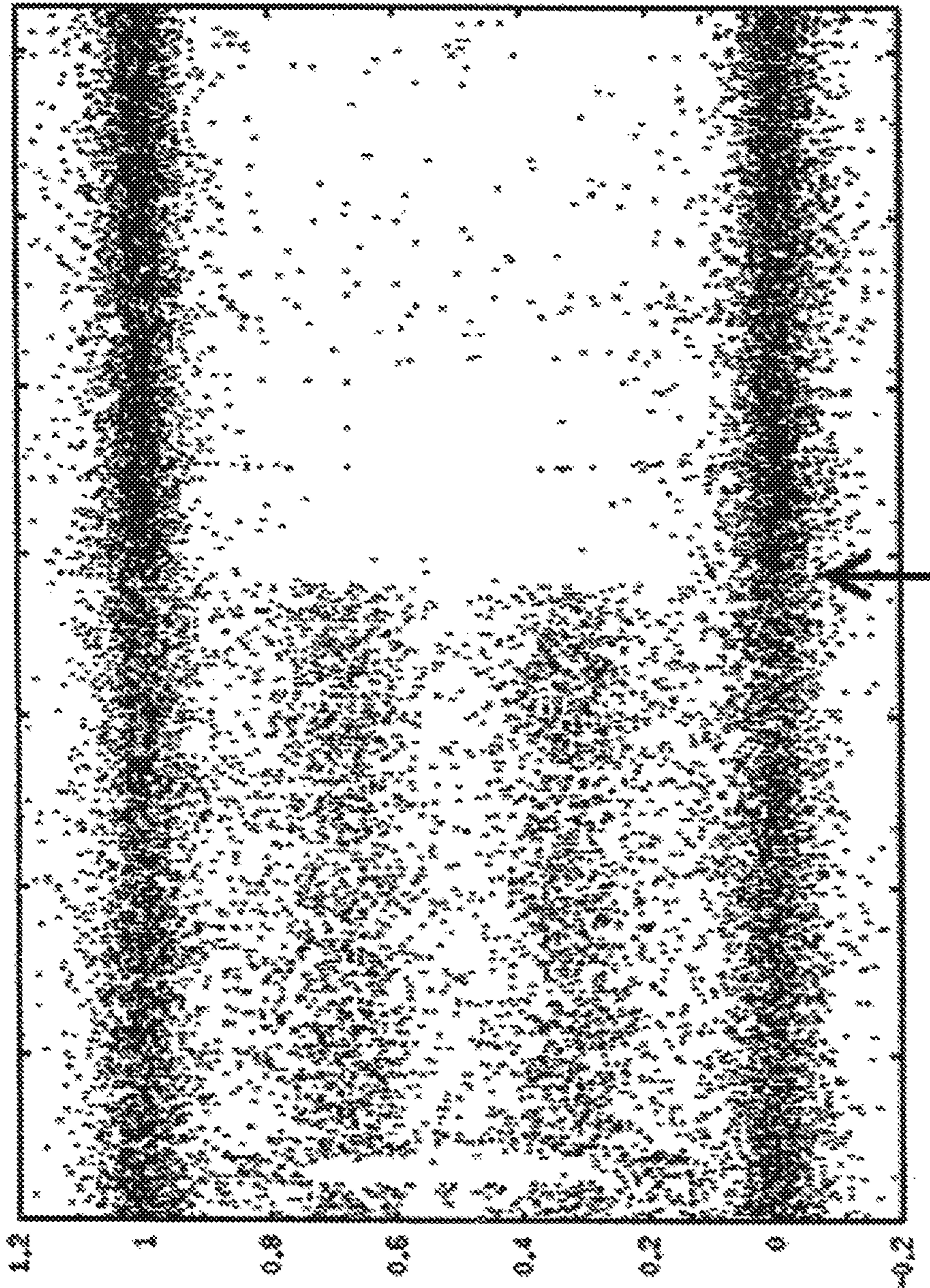
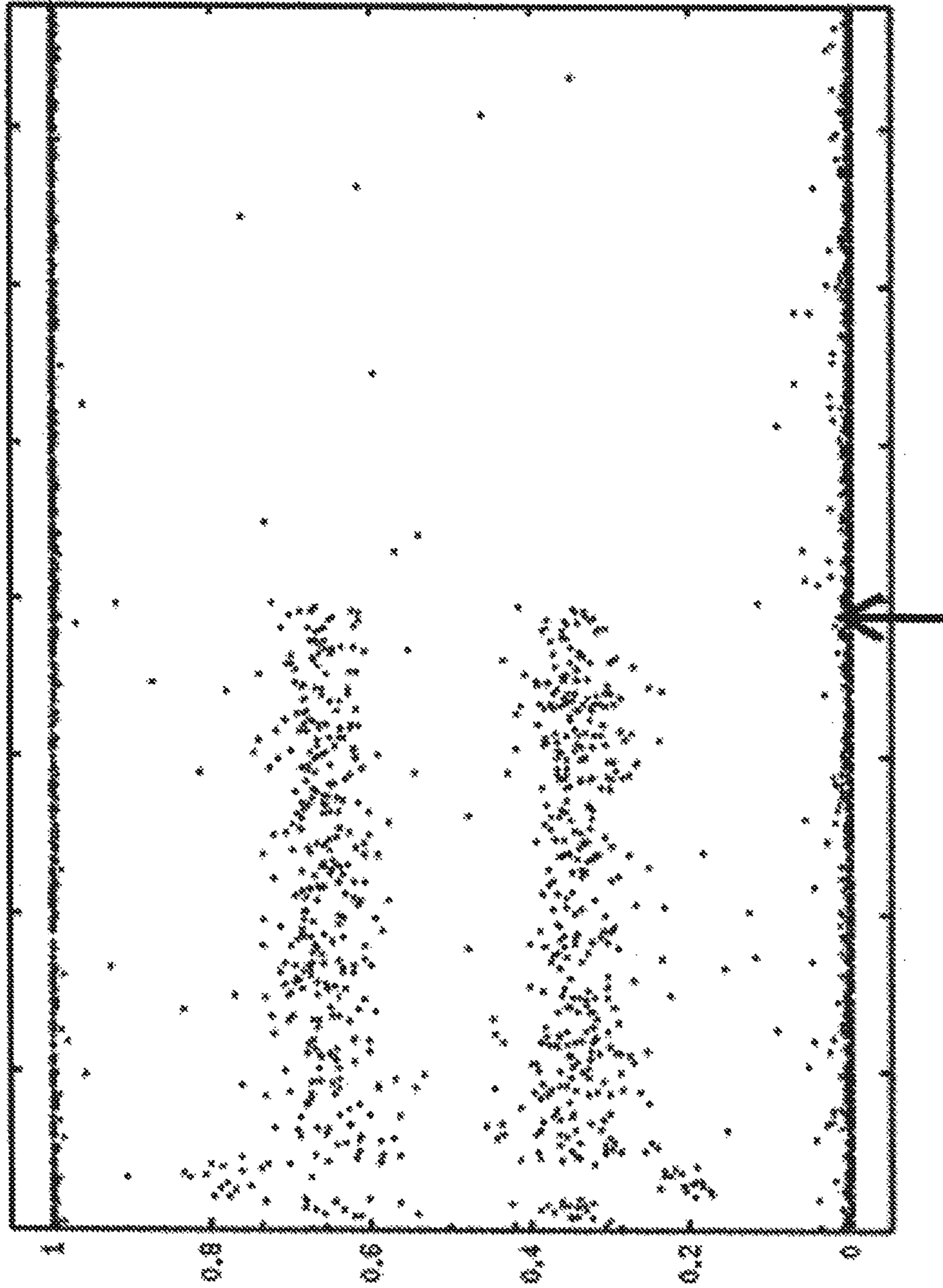


Figure 2



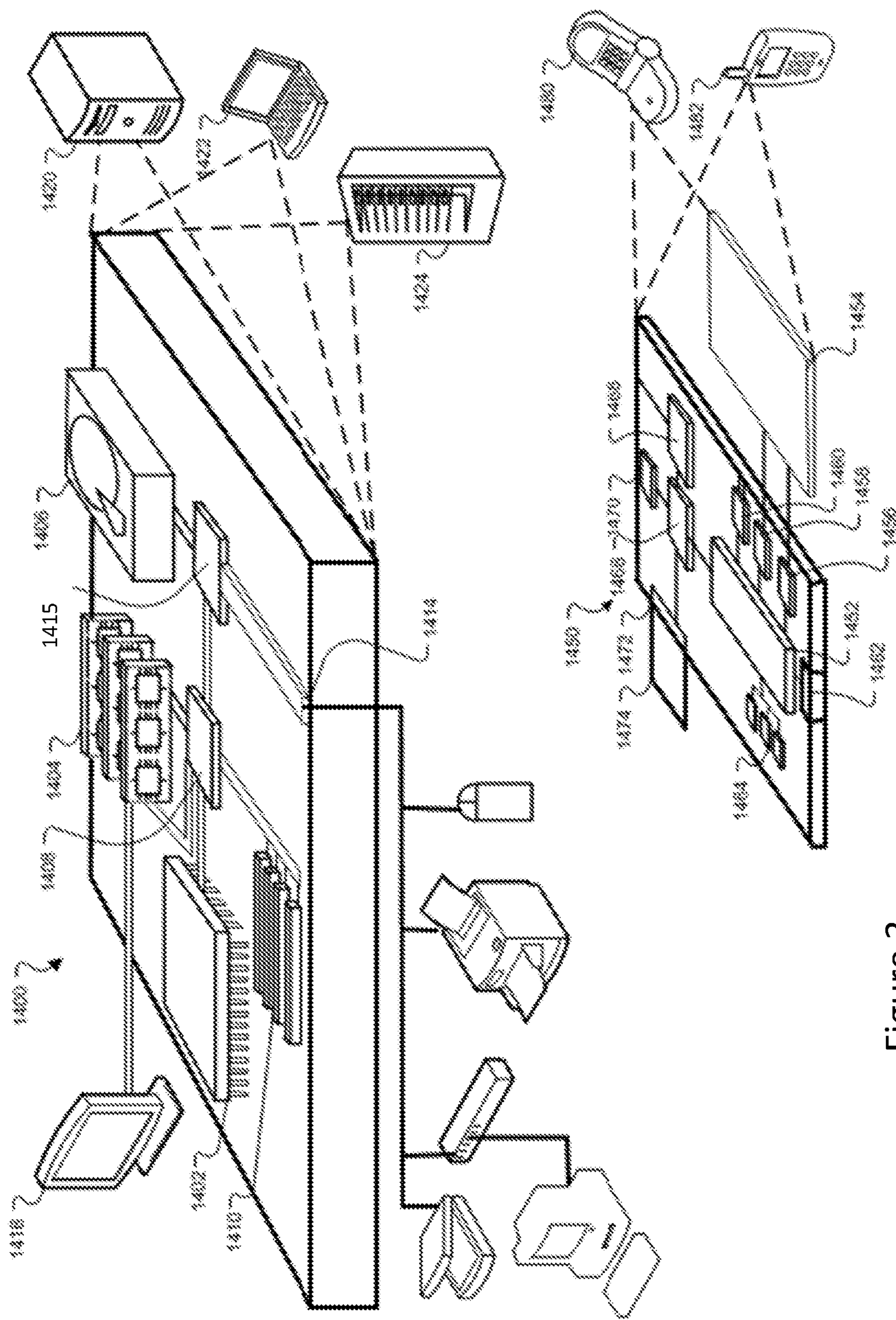


Figure 3

1**METHODS AND MATERIALS FOR
ASSESSING ALLELIC IMBALANCE****CROSS-REFERENCE TO RELATED
APPLICATIONS**

This application is a continuation of U.S. application Ser. No. 15/412,404, filed Jan. 23, 2017, which is a continuation of U.S. application Ser. No. 15/010,721, filed Jan. 29, 2016 (issued as U.S. Pat. No. 9,574,229), which is a continuation of U.S. application Ser. No. 14/109,163, filed Dec. 17, 2013 (issued as U.S. Pat. No. 9,279,156), which is a continuation of International Application No. PCT/US12/042668, filed Jun. 15, 2012, which claims the priority benefit of U.S. Provisional Application No. 61/498,418, filed Jun. 17, 2011, the entire contents of each of which are hereby incorporated by reference.

FIELD OF THE INVENTION

The invention generally relates to molecular diagnosis, and particularly to a method and system for detecting allelic imbalance in patient samples.

BACKGROUND OF THE INVENTION

In general, a comparison of sequences present at the same locus on each chromosome (each autosomal chromosome for males) of a chromosome pair can reveal whether that particular locus is homozygous or heterozygous within the genome of a cell. Polymorphic loci within the human genome are generally heterozygous within an individual since that individual typically receives one copy from the biological father and one copy from the biological mother. In some cases, a polymorphic locus or a string of polymorphic loci within an individual are homozygous as a result in inheriting identical copies from both biological parents. In other cases, homozygosity results from a loss of heterozygosity (LOH) from the germline. Because LOH and copy number information can be clinically useful, there is a need for improved methods of identifying loci and regions of LOH in samples.

BRIEF SUMMARY OF THE INVENTION

Copy number (including allelic imbalance and LOH) analysis of tumor tissues has been traditionally performed using single nucleotide polymorphism (SNP) arrays. The data quality is often highly variable and, especially for FFPE samples, tends to be poor. The inventors have developed a method of genome-wide copy number analysis that produces high quality data from all sample types that is based on in-solution capture of DNA fragments spanning target loci (e.g., SNPs), followed by parallel sequencing to identify and quantitate the alleles. The resulting data allows high quality LOH and copy number analysis of the sample.

Accordingly, in one aspect of the present invention, a method of detecting allelic imbalance status in a plurality of genomic loci in a tumor sample from a cancer patient is provided, comprising the steps of enriching a genomic DNA sample for DNA molecules each comprising a locus of interest; sequencing said DNA molecules to determine the genotype at each such locus; determining for each locus whether there is allelic imbalance.

In another aspect of the present invention, a method of detecting LOH status in a plurality of genomic loci in a tumor sample from a cancer patient is provided, comprising

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the steps of enriching a genomic DNA sample for DNA molecules each comprising a locus of interest; sequencing said DNA molecules to determine the genotype at each such locus; determining for each homozygous locus whether it is homozygous due to LOH.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention pertains. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable methods and materials are described below. In case of conflict, the present specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

Other features and advantages of the invention will be apparent from the following detailed description, and from the claims.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1 is a graph plotting allele dosages of breast cancer cells from a breast cancer patient along chromosome 1 as determined using a SNP array. The chromosome region between the arrows is an LOH region that is about 103 Mb in length.

FIG. 2 is a graph plotting allele dosages of breast cancer cells for the same breast cancer patient as on FIG. 1 along chromosome 1 as determined using high-throughput sequencing. The chromosome region between the arrows is an LOH region that is about 103 Mb in length.

FIG. 3 is a diagram of an example of a computer device and a mobile computer device that can be used to implement the techniques described herein.

**DETAILED DESCRIPTION OF THE
INVENTION**

It has been surprisingly discovered that determining allelic imbalance (e.g., abnormal copy number, LOH) in formalin-fixed paraffin-embedded (“FFPE”) samples using sequencing of genomic regions comprising loci of interest (e.g., SNPs) yields far superior quality data when compared to copy number and allelic imbalance data generated using microarrays. This invention enables large-scale (e.g., whole genome) copy number (e.g., allelic imbalance) analysis of samples of varying quality. In particular, it enables high quality data to be produced from FFPE-derived DNA. Current array-based platforms are unable to produce data of sufficient quality from this sample type.

Accordingly, in one aspect of the present invention, a method of detecting allelic imbalance status in a plurality of genomic loci in a tumor sample from a cancer patient is provided, comprising the steps of enriching a genomic DNA sample for DNA molecules each comprising a locus of interest; sequencing said DNA molecules to determine the genotype at each such locus; determining for each locus whether there is allelic imbalance. “Locus” as used herein has its usual meaning in the art. As used herein, “region” means a plurality of substantially adjacent loci. Unless stated otherwise or unless the context clearly indicates otherwise, statements made about a locus will generally apply to a region.

As used herein, “allelic imbalance” means any instance where the somatic copy number differs from the germline copy number at a genomic locus or region. In some embodiments allelic imbalance is expressed in terms of major copy

proportion (“MCP”). Major copy proportion and MCP, as used herein, mean the ratio of the major allele copy number to the major+minor allele copy number, as follows:

$$\text{MCP} = \frac{[\text{major allele copy number}]}{([\text{major allele copy number}] + [\text{minor allele copy number}])}$$

In some embodiments, a locus or region shows allelic imbalance if the MCP at such locus or region is 0.51, 0.52, 0.53, 0.54, 0.55, 0.6, 0.65, 0.7, 0.75, 0.8, 0.85, 0.9, 0.95, or 1.

One example of allelic imbalance is loss of heterozygosity (“LOH”), in which a locus is heterozygous in the germline but homozygous in somatic tissue. In this sense, homozygosity can include homozygous loss (i.e., deletion) of the locus in somatic tissue. The different types of possible LOH and allelic imbalance are discussed in more detail below.

Thus in some embodiments the present invention provides a method of detecting LOH status in a plurality of genomic loci in a tumor sample from a cancer patient, comprising enriching a genomic DNA sample for DNA molecules each comprising a locus of interest; sequencing said DNA molecules to determine the genotype at each such locus; determining for each homozygous locus whether it is homozygous due to LOH.

According to the present invention, nucleic acid sequencing techniques can be used to identify loci and/or regions as having allelic imbalance. For example, genomic DNA from a cell sample (e.g., a cancer cell sample) can be extracted and fragmented. Any appropriate method can be used to extract and fragment genomic nucleic acid including, without limitation, commercial kits such as QIAamp DNA Mini Kit (Qiagen), MagNA Pure DNA Isolation Kit (Roche Applied Science) and GenElute Mammalian Genomic DNA Miniprep Kit (Sigma-Aldrich). Once extracted and fragmented, either targeted or untargeted sequencing can be done to determine the sample’s genotypes at loci of interest. For example, whole genome, whole transcriptome, or whole exome sequencing can be done to determine genotypes at millions or even billions of base pairs (i.e., base pairs can be “loci” to be evaluated).

In some cases, targeted sequencing of known polymorphic loci (e.g., SNPs and surrounding sequences) can be done as an alternative to microarray analysis. For example, the genomic DNA can be enriched for those fragments containing a locus (e.g., SNP location) to be analyzed using kits designed for this purpose (e.g., Agilent SureSelect, Illumina TruSeq Capture, Nimblegen SeqCap EZ Choice, Raindance Thunderstorm™). For example, genomic DNA containing the loci to be analyzed can be hybridized to biotinylated capture RNA fragments to form biotinylated RNA/genomic DNA complexes. Alternatively, DNA capture probes may be utilized resulting in the formation of biotinylated DNA/genomic DNA hybrids. Streptavidin coated magnetic beads and a magnetic force can be used to separate the biotinylated RNA/genomic DNA complexes from those genomic DNA fragments not present within a biotinylated RNA/genomic DNA complex. The obtained biotinylated RNA/genomic DNA complexes can be treated to remove the captured RNA from the magnetic beads, thereby leaving intact genomic DNA fragments containing a locus to be analyzed. These intact genomic DNA fragments containing the loci to be analyzed can be amplified using, for example, PCR techniques. Alternatively, a multiplex PCR reaction can be employed to enrich for loci of interest. PCR primers can be designed to flank loci of interest and a PCR reaction can be run to amplify sequences comprising such loci.

The enriched genomic DNA fragments can be sequenced using any sequencing technique. Beyond Sanger sequencing, numerous suitable sequencing machines and strategies are well known in the art, including but not limited to those developed by Illumina (the Genome Analyzer; Bennett et al. (2005) *Pharmacogenomics*, 6:373-382; HiSeq; MiSeq); by Applied Biosystems, Inc. (the SOLiD™ Sequencer; solid.appliedbiosystems.com); by Roche (e.g., the 454 GS FLX™ sequencer; Margulies et al. (2005) *Nature*, 437:376-380; U.S. Pat. Nos. 6,274,320; 6,258,568; 6,210,891); by Helicos Biosciences (Heliscope™ system, see, e.g., U.S. Patent App. Pub. No. 2007/0070349); by Oxford Nanopore (e.g., GridION™ and MinION™, see, e.g., International Application No. PCT/GB2009/001690, pub. no. WO/2010/004273); and by others.

The sequencing results from the genomic DNA fragments can be used to identify loci as having allelic imbalance. In some cases, an analysis of the allelic imbalance status of loci over a length of a chromosome can be performed to determine the length of regions of allelic imbalance. For example, a stretch of SNP locations that are spaced apart (e.g., spaced about 25 kb to about 100 kb apart) along a chromosome can be evaluated by sequencing, and the sequencing results used to determine not only the presence of a region of allelic imbalance () e.g., somatic homozygosity) along a chromosome but also the length of that region of imbalance. Obtained sequencing results can be used to generate a graph that plots allele dosages along a chromosome. Allele dosage d_i for SNP i can be calculated from the adjusted number of captured probes for two alleles (A_i and B_i): $d_i = A_i / (A_i + B_i)$. An example of such a graph is presented in FIG. 2.

Once a sample’s genotype (e.g., homozygosity) has been determined for a plurality of loci (e.g., SNPs), common techniques can be used to identify loci and regions of allelic imbalance due to somatic change (e.g., LOH). One way to determine whether imbalance is due to somatic change is to compare the somatic genotype to the germline. For example, the genotype for a plurality of loci (e.g., SNPs) can be determined in both a germline (e.g., blood) sample and a somatic (e.g., tumor) sample. The genotypes for each sample can be compared (typically computationally) to determine where the genome of the germline cell was, e.g., heterozygous and the genome of the somatic cell is, e.g., homozygous. Such loci are LOH loci and regions of such loci are LOH regions.

Computational techniques can also be used to determine whether allelic imbalance is somatic (e.g., due to LOH). Such techniques are particularly useful when a germline sample is not available for analysis and comparison. For example, algorithms such as those described elsewhere can be used to detect allelic imbalance regions using information from SNP arrays (Nannya et al., *Cancer Res.*, 65:6071-6079 (2005)). Typically these algorithms do not explicitly take into account contamination of tumor samples with benign tissue. Cf. International Application No. PCT/US2011/026098 to Abkevich et al.; Goransson et al., *PLoS One* (2009) 4(6):e6057. This contamination is often high enough to make the detection of allelic imbalance regions challenging. Improved analytical methods according to the present invention for identifying allelic imbalance, even in spite of contamination, include those embodied in computer software products as described below.

The following is one example. If the observed ratio (e.g., MCP) of the signals of two alleles, A and B, is two to one, there are two possibilities. The first possibility is that cancer cells have LOH with deletion of allele B in a sample with 50% contamination with normal cells. The second possibil-

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ity is that there is no LOH but allele A is duplicated in a sample with no contamination with normal cells. An algorithm can be implemented as a computer program as described herein to reconstruct LOH regions based on genotype (e.g., SNP genotype) data. One point of the algorithm is to first reconstruct allele specific copy numbers (ASCN) at each locus (e.g., SNP). ASCNs are the numbers of copies of both paternal and maternal alleles. An LOH region is then determined as a stretch of SNPs with one of the ASCNs (paternal or maternal) being zero. The algorithm can be based on maximizing a likelihood function and can be conceptually akin to a previously described algorithm designed to reconstruct total copy number (rather than ASCN) at each locus (e.g., SNP). See International Application No. PCT/US2011/026098 (pub. no. WO/2011/106541) (hereby incorporated by reference in its entirety). The likelihood function can be maximized over ASCN of all loci, level of contamination with benign tissue, total copy number averaged over the whole genome, and sample specific noise level. The input data for the algorithm can include or consist of (1) sample-specific normalized signal intensities for both allele of each locus and (2) assay-specific (specific for different SNP arrays and for sequence based approach) set of parameters defined based on analysis of large number of samples with known ASCN profiles.

In some cases, a selection process can be used to select loci (e.g., SNP loci) to be evaluated using an assay configured to identify loci as having allelic imbalance (e.g., SNP array-based assays and sequencing-based assays). For example, any human SNP location can be selected for inclusion in a SNP array-based assay or a sequencing-based assay configured to identify loci as having allelic imbalance within the genome of cells. In some cases, 0.5, 1.0, 1.5, 2.0, 2.5 million or more loci (e.g., SNP locations) present within the human genome can be evaluated to identify those loci that (a) are not present on the Y chromosome, (b) are not mitochondrial loci, (c) have a minor allele frequency of at least about 5% in the population of interest (e.g., Caucasians), (d) have a minor allele frequency of at least about 1% in three populations other than the population of interest (e.g., Chinese, Japanese, and Yoruba), and/or (e) do not have a significant deviation from Hardy-Weinberg equilibrium in any of these populations. In some cases, more than 100,000, 150,000, or 200,000 human loci can be selected that meet criteria (a) through (e). Of the human loci meeting criteria (a) through (e), a group of loci (e.g., top 2,500, 5,000, 7,500, 10,000, 20,000, 30,000, 40,000, 50,000, 75,000, 100,000, 150,000, or 200,000 loci) can be selected such that the loci have a high degree of allele frequency in the population of interest, cover the human genome in a somewhat evenly spaced manner (e.g., at least one locus of interest every about 5 kb, 10 kb, 25 kb, 50 kb, 75 kb, 100 kb, 150 kb, 200 kb, 300 kb, 400 kb, 500 kb or more), and are not in linkage disequilibrium with another selected locus in any of the populations used for analysis. In some cases, about 40, 50, 60, 70, 80, 90, 100, 110, 120, 130 thousand or more loci can be selected as meeting each of these criteria and included in an assay configured to identify allelic imbalance regions across a human genome. For example, between about 70,000 and about 90,000 (e.g., about 80,000) SNPs can be selected for analysis with a SNP array-based assay, and between about 45,000 and about 55,000 (e.g., about 54,000) SNPs can be selected for analysis with a sequencing-based assay.

Accordingly, in one aspect of the present invention, a method of detecting allelic imbalance status in a plurality of genomic loci in a sample from a patient is provided, com-

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prising the steps of enriching a genomic DNA sample for DNA molecules each comprising a locus of interest; sequencing said DNA molecules to determine the genotype at each such locus; determining for each locus whether it has allelic imbalance.

In another aspect of the present invention, a method of detecting LOH status in a plurality of genomic loci in a sample from a patient is provided, comprising the steps of enriching a genomic DNA sample for DNA molecules each comprising a locus of interest; sequencing said DNA molecules to determine the genotype at each such locus; determining for each homozygous locus whether it is homozygous due to LOH.

In another aspect of the present invention, a method of detecting copy number status in a plurality of genomic loci in a sample from a patient is provided, comprising the steps of enriching a genomic DNA sample for DNA molecules each comprising a locus of interest; sequencing said DNA molecules; and quantitating each allele at each such locus to determine its copy number.

In some embodiments at least 10, 50, 100, 1,000, 10,000, 50,000, 55,000, 75,000, 100,000, 150,000, 200,000, 300,000, 400,000, 500,000, 750,000, 1,000,000, 2,000,000 or more loci are evaluated. In some embodiments these loci are spaced evenly along the genome. As used herein, loci are “evenly spaced along the genome” when the percentage difference between the distance_{AB} between any two loci A and B and the distance_{CD} between any other two loci C and D (i.e., $100 * (\text{distance}_{AB} - \text{distance}_{CD}) / \text{distance}_{AB}$ or $100 * (\text{distance}_{AB} - \text{distance}_{CD}) / \text{distance}_{CD}$) is less than or equal to 50%, 40%, 30%, 20%, 15%, 10%, 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2%, or 1%. Such percentage difference is referred to herein as the “genomic spacing” of loci. In some embodiments the sample is an FFPE tissue sample. In some embodiments the sample is a tumor sample from the patient.

Another aspect of the invention provides a system for determining allelic imbalance status in a plurality of loci in a sample comprising: a sample analyzer for (1) enriching a genomic DNA sample for DNA molecules each comprising a locus of interest and (2) sequencing said DNA molecules to produce a plurality of quantitative signals about each such locus; a computer program for analyzing said plurality of quantitative signals to determine whether each such locus has allelic imbalance.

Another aspect of the invention provides a system for determining LOH status in a plurality of loci in a sample comprising: a sample analyzer for (1) enriching a genomic DNA sample for DNA molecules each comprising a locus of interest and (2) sequencing said DNA molecules to produce a plurality of quantitative signals about each such locus; a computer program for analyzing said plurality of quantitative signals to determine whether each such locus is homozygous in the sample; and a computer program for determining for each homozygous locus whether it is homozygous due to LOH.

Another aspect of the invention provides a system for detecting copy number status in a plurality of genomic loci in a sample from a patient comprising: a sample analyzer for (1) enriching a genomic DNA sample for DNA molecules each comprising a locus of interest and (2) sequencing said DNA molecules to produce a plurality of quantitative signals about each such locus; and a computer program for analyzing said plurality of quantitative signals to quantitate each allele at each such locus to determine its copy number.

In some embodiments of the systems of the invention, one sample analyzer both enriches the sample for DNA of interest and sequences that DNA. In other embodiments two

or more sample analyzers perform these functions. In some embodiments, one software program analyzes the plurality of quantitative signals to determine whether each locus is homozygous in the sample and also determines for each homozygous locus whether it is homozygous due to LOH.

FIG. 3 is a diagram of an example of a computer device **1400** and a mobile computer device **1450**, which may be used with the techniques described herein. Computing device **1400** is intended to represent various forms of digital computers, such as laptops, desktops, workstations, personal digital assistants, servers, blade servers, mainframes, and other appropriate computers. Computing device **1450** is intended to represent various forms of mobile devices, such as personal digital assistants, cellular telephones, smart phones, and other similar computing devices. The components shown here, their connections and relationships, and their functions, are meant to be exemplary only, and are not meant to limit implementations of the inventions described and/or claimed in this document.

Computing device **1400** includes a processor **1402**, memory **1404**, a storage device **1406**, a high-speed interface **1408** connecting to memory **1404** and high-speed expansion ports **1410**, and a low speed interface **1415** connecting to low speed bus **1414** and storage device **1406**. Each of the components **1402**, **1404**, **1406**, **1408**, **1410**, and **1415**, are interconnected using various busses, and may be mounted on a common motherboard or in other manners as appropriate. The processor **1402** can process instructions for execution within the computing device **1400**, including instructions stored in the memory **1404** or on the storage device **1406** to display graphical information for a GUI on an external input/output device, such as display **1416** coupled to high speed interface **1408**. In other implementations, multiple processors and/or multiple buses may be used, as appropriate, along with multiple memories and types of memory. Also, multiple computing devices **1400** may be connected, with each device providing portions of the necessary operations (e.g., as a server bank, a group of blade servers, or a multi-processor system).

The memory **1404** stores information within the computing device **1400**. In one implementation, the memory **1404** is a volatile memory unit or units. In another implementation, the memory **1404** is a non-volatile memory unit or units. The memory **1404** may also be another form of computer-readable medium, such as a magnetic or optical disk.

The storage device **1406** is capable of providing mass storage for the computing device **1400**. In one implementation, the storage device **1406** may be or contain a computer-readable medium, such as a floppy disk device, a hard disk device, an optical disk device, or a tape device, a flash memory or other similar solid state memory device, or an array of devices, including devices in a storage area network or other configurations. A computer program product can be tangibly embodied in an information carrier. The computer program product may also contain instructions that, when executed, perform one or more methods, such as those described herein. The information carrier is a computer- or machine-readable medium, such as the memory **1404**, the storage device **1406**, memory on processor **1402**, or a propagated signal.

The high speed controller **1408** manages bandwidth-intensive operations for the computing device **1400**, while the low speed controller **1415** manages lower bandwidth-intensive operations. Such allocation of functions is exemplary only. In one implementation, the high-speed controller **1408** is coupled to memory **1404**, display **1416** (e.g.,

through a graphics processor or accelerator), and to high-speed expansion ports **1410**, which may accept various expansion cards (not shown). In the implementation, low-speed controller **1415** is coupled to storage device **1406** and low-speed expansion port **1414**. The low-speed expansion port, which may include various communication ports (e.g., USB, Bluetooth, Ethernet, or wireless Ethernet) may be coupled to one or more input/output devices, such as a keyboard, a pointing device, a scanner, an optical reader, a fluorescent signal detector, or a networking device such as a switch or router, e.g., through a network adapter.

The computing device **1400** may be implemented in a number of different forms, as shown in the figure. For example, it may be implemented as a standard server **1420**, or multiple times in a group of such servers. It may also be implemented as part of a rack server system **1424**. In addition, it may be implemented in a personal computer such as a laptop computer **1422**. Alternatively, components from computing device **1400** may be combined with other components in a mobile device (not shown), such as device **1450**. Each of such devices may contain one or more of computing device **1400**, **1450**, and an entire system may be made up of multiple computing devices **1400**, **1450** communicating with each other.

Computing device **1450** includes a processor **1452**, memory **1464**, an input/output device such as a display **1454**, a communication interface **1466**, and a transceiver **1468**, among other components (e.g., a scanner, an optical reader, a fluorescent signal detector). The device **1450** may also be provided with a storage device, such as a microdrive or other device, to provide additional storage. Each of the components **1450**, **1452**, **1464**, **1454**, **1466**, and **1468**, are interconnected using various buses, and several of the components may be mounted on a common motherboard or in other manners as appropriate.

The processor **1452** can execute instructions within the computing device **1450**, including instructions stored in the memory **1464**. The processor may be implemented as a chipset of chips that include separate and multiple analog and digital processors. The processor may provide, for example, for coordination of the other components of the device **1450**, such as control of user interfaces, applications run by device **1450**, and wireless communication by device **1450**.

Processor **1452** may communicate with a user through control interface **1458** and display interface **1456** coupled to a display **1454**. The display **1454** may be, for example, a TFT LCD (Thin-Film-Transistor Liquid Crystal Display) or an OLED (Organic Light Emitting Diode) display, or other appropriate display technology. The display interface **1456** may comprise appropriate circuitry for driving the display **1454** to present graphical and other information to a user. The control interface **1458** may receive commands from a user and convert them for submission to the processor **1452**. In addition, an external interface **1462** may be provide in communication with processor **1452**, so as to enable near area communication of device **1450** with other devices. External interface **1462** may provide, for example, for wired communication in some implementations, or for wireless communication in other implementations, and multiple interfaces may also be used.

The memory **1464** stores information within the computing device **1450**. The memory **1464** can be implemented as one or more of a computer-readable medium or media, a volatile memory unit or units, or a non-volatile memory unit or units. Expansion memory **1474** may also be provided and connected to device **1450** through expansion interface **1472**,

which may include, for example, a SIMM (Single In Line Memory Module) card interface. Such expansion memory **1474** may provide extra storage space for device **1450**, or may also store applications or other information for device **1450**. For example, expansion memory **1474** may include instructions to carry out or supplement the processes described herein, and may include secure information also. Thus, for example, expansion memory **1474** may be provide as a security module for device **1450**, and may be programmed with instructions that permit secure use of device **1450**. In addition, secure applications may be provided via the SIMM cards, along with additional information, such as placing identifying information on the SIMM card in a non-hackable manner.

The memory may include, for example, flash memory and/or NVRAM memory, as discussed below. In one implementation, a computer program product is tangibly embodied in an information carrier. The computer program product contains instructions that, when executed, perform one or more methods, such as those described herein. The information carrier is a computer- or machine-readable medium, such as the memory **1464**, expansion memory **1474**, memory on processor **1452**, or a propagated signal that may be received, for example, over transceiver **1468** or external interface **1462**.

Device **1450** may communicate wirelessly through communication interface **1466**, which may include digital signal processing circuitry where necessary. Communication interface **1466** may provide for communications under various modes or protocols, such as GSM voice calls, SMS, EMS, or MMS messaging, CDMA, TDMA, PDC, WCDMA, CDMA2000, or GPRS, among others. Such communication may occur, for example, through radio-frequency transceiver **1468**. In addition, short-range communication may occur, such as using a Bluetooth, WiFi, or other such transceiver (not shown). In addition, GPS (Global Positioning System) receiver module **1470** may provide additional navigation- and location-related wireless data to device **1450**, which may be used as appropriate by applications running on device **1450**.

Device **1450** may also communicate audibly using audio codec **1460**, which may receive spoken information from a user and convert it to usable digital information. Audio codec **1460** may likewise generate audible sound for a user, such as through a speaker, e.g., in a handset of device **1450**. Such sound may include sound from voice telephone calls, may include recorded sound (e.g., voice messages, music files, etc.) and may also include sound generated by applications operating on device **1450**.

The computing device **1450** may be implemented in a number of different forms, as shown in the figure. For example, it may be implemented as a cellular telephone **1480**. It may also be implemented as part of a smartphone **1482**, personal digital assistant, or other similar mobile device.

Various implementations of the systems and techniques described herein can be realized in digital electronic circuitry, integrated circuitry, specially designed ASICs (application specific integrated circuits), computer hardware, firmware, software, and/or combinations thereof. These various implementations can include implementation in one or more computer programs that are executable and/or interpretable on a programmable system including at least one programmable processor, which may be special or general purpose, coupled to receive data and instructions

from, and to transmit data and instructions to, a storage system, at least one input device, and at least one output device.

These computer programs (also known as programs, software, software applications or code) include machine instructions for a programmable processor, and can be implemented in a high-level procedural and/or object-oriented programming language, and/or in assembly/machine language. As used herein, the terms “machine-readable medium” and “computer-readable medium” refer to any computer program product, apparatus and/or device (e.g., magnetic discs, optical disks, memory, and Programmable Logic Devices (PLDs)) used to provide machine instructions and/or data to a programmable processor, including a machine-readable medium that receives machine instructions as a machine-readable signal. The term “machine-readable signal” refers to any signal used to provide machine instructions and/or data to a programmable processor.

To provide for interaction with a user, the systems and techniques described herein can be implemented on a computer having a display device (e.g., a CRT (cathode ray tube) or LCD (liquid crystal display) monitor) for displaying information to the user and a keyboard and a pointing device (e.g., a mouse or a trackball) by which the user can provide input to the computer. Other kinds of devices can be used to provide for interaction with a user as well; for example, feedback provided to the user can be any form of sensory feedback (e.g., visual feedback, auditory feedback, or tactile feedback); and input from the user can be received in any form, including acoustic, speech, or tactile input.

The systems and techniques described herein can be implemented in a computing system that includes a back end component (e.g., as a data server), or that includes a middleware component (e.g., an application server), or that includes a front end component (e.g., a client computer having a graphical user interface or a Web browser through which a user can interact with an implementation of the systems and techniques described herein), or any combination of such back end, middleware, or front end components. The components of the system can be interconnected by any form or medium of digital data communication (e.g., a communication network). Examples of communication networks include a local area network (“LAN”), a wide area network (“WAN”), and the Internet.

The computing system can include clients and servers. A client and server are generally remote from each other and typically interact through a communication network. The relationship of client and server arises by virtue of computer programs running on the respective computers and having a client-server relationship to each other.

In some cases, a system provided herein can be configured to include one or more sample analyzers. A sample analyzer can be configured to produce a plurality of signals about genomic DNA of a cancer cell. For example, a sample analyzer can produce signals that are capable of being interpreted in a manner that identifies the allelic imbalance status of loci along a chromosome. In some cases, a sample analyzer can be configured to carry out one or more steps of a sequencing-based assay and can be configured to produce and/or capture signals from such assays. In some cases, a computing system provided herein can be configured to include a computing device. In such cases, the computing device can be configured to receive signals from a sample analyzer.

The computing device can include computer-executable instructions or a computer program (e.g., software) containing computer-executable instructions for carrying out one or

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more of the methods or steps described herein. In some cases, such computer-executable instructions can instruct a computing device to analyze signals from a sample analyzer, from another computing device, or from a sequencing-based assay. The analysis of such signals can be carried out to determine genotypes, allelic imbalance at certain loci, regions of allelic imbalance, the number of allelic imbalance regions, to determine the size of allelic imbalance regions, to determine the number of allelic imbalance regions having a particular size or range of sizes, or to determine a combination of these items.

In some cases, a system provided herein can include computer-executable instructions or a computer program (e.g., software) containing computer-executable instructions for formatting an output providing an indication about copy number, allelic imbalance, LOH, or a combination of these items.

In some cases, a system provided herein can include a pre-processing device configured to process a sample (e.g., cancer cells) such that a sequencing-based assay can be performed. Examples of pre-processing devices include, without limitation, devices configured to enrich cell populations for cancer cells as opposed to non-cancer cells, devices configured to lyse cells and/or extract genomic nucleic acid, and devices configured to enrich a sample for particular genomic DNA fragments.

Additional embodiments of the invention are as follows:

Embodiment 1

An in vitro method of detecting allelic imbalance status in a plurality of genomic loci in a sample from a patient, comprising:

- enriching a genomic DNA sample for DNA molecules each comprising a locus of interest;
- sequencing said DNA molecules to determine the genotype at each such locus;
- determining for each locus whether it has allelic imbalance.

Embodiment 2

An in vitro method of detecting LOH status in a plurality of genomic loci in a sample from a patient, comprising:

- enriching a genomic DNA sample for DNA molecules each comprising a locus of interest;
- sequencing said DNA molecules to determine the genotype at each such locus;
- determining for each homozygous locus whether it is homozygous due to LOH.

Embodiment 3

A system for determining allelic imbalance status in a plurality of genomic loci in a sample comprising:

- a sample analyzer for (1) enriching a genomic DNA sample for DNA molecules each comprising a locus of interest and (2) sequencing said DNA molecules to produce a plurality of quantitative signals about each such locus;
- a computer program for analyzing said plurality of quantitative signals to determine the genotype of each such locus in the sample; and
- a computer program for determining for each locus whether it has allelic imbalance.

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A system for determining LOH status in a plurality of genomic loci in a sample comprising:

- a sample analyzer for (1) enriching a genomic DNA sample for DNA molecules each comprising a locus of interest and (2) sequencing said DNA molecules to produce a plurality of quantitative signals about each such locus;
- a computer program means for analyzing said plurality of quantitative signals to determine the genotype of each such locus in the sample; and
- a computer means for determining for each homozygous locus whether it is homozygous due to LOH.

Embodiment 5

The method of either Embodiment 1 or Embodiment 2 or the system of either Embodiment 3 or Embodiment 4, wherein said plurality of genomic loci comprises at least 10, 50, 100, 1,000, 10,000, 50,000, 55,000, 75,000, 100,000, 150,000, 200,000, 300,000, 400,000, 500,000, 750,000, 1,000,000, or 2,000,000 or more loci.

Embodiment 6

The method or system of Embodiment 5, wherein said genomic loci are evenly spaced along the genome.

Embodiment 7

The method or system of Embodiment 6, wherein the genomic spacing of said plurality of genomic loci is less than or equal to 50%, 40%, 30%, 20%, 15%, 10%, 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2%, or 1%.

Embodiment 8

The method of either Embodiment 1 or Embodiment 2 or the system of either Embodiment 3 or Embodiment 4, wherein said sample is a formalin-fixed, paraffin-embedded tissue sample.

Embodiment 9

The method or system of Embodiment 8, wherein said sample is a tumor sample extracted from the patient.

Examples

The process described here utilized an Agilent SureSelect Capture system followed by Illumina HiSeq sequencing, however any in solution or solid support based capture method and high throughput parallel sequencing platform could be used.

The initial design selection process utilized the ~2.5 million SNPs on the Illumina Omni2.5 SNP array. This list of SNPs was chosen because it is the currently the largest list of SNPs from which there is genotyping information available for multiple different population groups. All 2,448,785 SNP locations were input into the Agilent eArray Sure Select Target Enrichment wizard for Single End Long Reads using the default settings. 1,353,042 passed the selection criteria and had baits designed.

Then, 110,000 SNPs with high minor allele frequencies and evenly covering the genome were selected. In the

selection, SNPs in strong linkage disequilibrium and SNPs with strong deviation from Hardy-Weinberg equilibrium were discarded.

Two preliminary library designs were constructed comprising of 55,000 probes each targeting 55,000 different SNP locations. Testing was carried out using a high quality normal DNA sample to check for even capture of both alleles of every SNP. In addition, 4 FFPE samples were captured and used to select the most optimally performing probes. We looked for probes that showed robust capture and even sequence depth without over or underrepresentation of sequence reads in the final sequencing library.

The final capture probe library design was comprised of the 55,000 optimal probes identified using the preliminary capture designs.

The results of measuring copy number and LOH using the above sequencing technique are shown in FIG. 2 (with FIG. 1 showing microarray analysis on fresh frozen tissue as a comparison).

All publications and patent applications mentioned in the specification are indicative of the level of those skilled in the art to which this invention pertains. All publications and patent applications are herein incorporated by reference to the same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated by reference. The mere mentioning of the publications and patent applications does not necessarily constitute an admission that they are prior art to the instant application.

Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be obvious that certain changes and modifications may be practiced within the scope of the appended claims.

What is claimed is:

1. An in vitro method of detecting loss of heterozygosity (LOH) status in a plurality of single nucleotide polymorphism (SNP) genomic loci in a formalin-fixed paraffin-embedded tissue sample from a patient, comprising:

enriching a genomic DNA sample for DNA molecules each comprising a SNP locus of interest, wherein there is at least one SNP locus located on average every 5 Mb within each chromosome that is examined;

sequencing the DNA molecules to determine the genotype at each such SNP locus;

determining for each homozygous SNP locus whether it is homozygous due to LOH.

2. The method of claim 1, wherein there is at least one SNP locus located on average every 1 Mb within each chromosome that is examined.

3. The method of claim 1, wherein the plurality of genomic SNP loci comprises at least 5,000 more loci.

4. The method of claim 1, wherein the plurality of genomic SNP loci comprises at least 10,000 more loci.

5. The method of claim 1, wherein a SNP locus is determined to have allelic imbalance if the major copy proportion at the SNP locus is 0.51 or greater.

6. The method of claim 1, wherein the SNP genomic loci are evenly spaced along the genome.

7. The method of claim 6, wherein the percentage difference between the distance between any two of the plurality of SNP genomic loci and the distance between any other two of the plurality of SNP loci is less than or equal to 20%.

8. The method of claim 1, wherein the sample is a tumor sample extracted from the patient.

9. The method of claim 8, wherein the tumor sample comprises at least 5%, or more contamination with non-tumor cells.

10. The method of claim 1, wherein there is at least one single nucleotide polymorphism locus located on average every 500 kb within each chromosome.

11. A system for determining LOH status in a plurality of SNP genomic loci in a formalin-fixed paraffin-embedded tissue sample, wherein the system comprises:

a sample analyzer configured to

enrich a genomic DNA sample for DNA molecules, each test DNA molecule comprising a SNP locus of interest and wherein there is at least one SNP locus located on average every 5 Mb within each chromosome that is examined;

sequencing the DNA molecules to produce a plurality of quantitative signals for each such SNP locus;

a computer program that is configured to analyze the plurality of quantitative signals to determine the genotype of each such SNP locus in the sample; and

a computer program that is configured to determine, for each homozygous SNP locus, whether the locus is homozygous due to LOH.

12. The system of claim 11, wherein there is at least one SNP locus located on average every 1 Mb within each chromosome that is examined.

13. The system of claim 11, wherein the plurality of genomic SNP loci comprises at least 5,000 more loci.

14. The system of claim 11, wherein the plurality of genomic SNP loci comprises at least 10,000 more loci.

15. The system of claim 11, wherein a SNP locus is determined to have allelic imbalance if the major copy proportion at the SNP locus is 0.51 or greater.

16. The system of claim 11, wherein the SNP genomic loci are evenly spaced along the genome.

17. The system of claim 16, wherein the percentage difference between the distance between any two of the plurality of SNP genomic loci and the distance between any other two of the plurality of SNP loci is less than or equal to 20%.

18. The system of claim 11, wherein the sample is a tumor sample extracted from the patient.

19. The system of claim 18, wherein the tumor sample comprises at least 5%, or more contamination with non-tumor cells.

20. The system of claim 11, wherein there is at least one single nucleotide polymorphism locus located on average every 500 kb within each chromosome.

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